AMENDMENTS TO THE CLAIMS

Listing of Claims

This listing of the claims will replace all prior versions, and listings, of claims in this application.

1 – 59. (**Cancelled**)

60. (**Currently Amended**) A method of identifying compounds that bind to a leukotriene A_4 (LTA_4) hydrolase comprising the amino acid sequence of SEQ ID NO:1, the method comprising the steps of:

(a) crystallizing a purified LTA_4 hydrolase in the presence of bestatin to form a co-crystal of [[an]] LTA_4 hydrolase and bestatin~~crystal~~, wherein crystallization is performed [[as]]by liquid-liquid diffusion in a capillary using equal volumes of a buffer: enzyme solution consisting of:

i) a buffer solution consisting of 28% PEG8000, 0.1 M Na-acetate, 0.1 M imidazole at a pH of 6.8 and with 5 mM $YbCl_3$ as an additive; and

ii) an enzyme solution consisting of 5 mg/ml LTA_4 hydrolase comprising the amino acid sequence of SEQ ID NO:1 in 10 mM Tris-HCl at a pH of 8, supplemented with 1 mM bestatin;

wherein the crystallization results in a LTA_4 hydrolase crystal having the space group $P2_12_12$ and the unit cell dimensions a=67.59 Å, b=133.51 Å, and c=83.40 Å and $\alpha=\beta=\gamma=90°$;

(b) determining the atomic coordinates of said LTA_4 hydrolase crystal; and

(c) screening the atomic coordinates of a set of candidate compounds against the atomic coordinates of said LTA_4 hydrolase crystal obtained in step a) to identify compounds that bind to the LTA_4 hydrolase~~;~~

~~wherein the crystallization results in a LTA_4 hydrolase crystal having the space group P21212 and the unit cell dimensions a=67.59 Å, b=133.51 Å, and c=83.40 Å and wherein $\alpha=\beta=\gamma=90°$~~.

61. (**Previously Presented**) The method of claim 60, wherein the LTA_4 hydrolase is purified by adsorption chromatography on hydroxyapatite and anion-exchange chromatography.

62-67. (**Cancelled**)

68. (**Previously Presented**) The method of claim 60, wherein the atomic coordinates of said LTA_4 hydrolase crystal correspond to the atomic coordinates defining atom 1 to atom 4876 as set forth in Table 9.

69. (**Cancelled**)

70. (**Currently Amended**) A method of designing an inhibitor or an agonist of LTA_4 hydrolase comprising the amino acid sequence of SEQ ID NO:1, the method comprising the steps of:

(a) crystallizing a purified LTA_4 hydrolase in the presence of bestatin to form a co-crystal of LTA_4 hydrolase and bestatin and thereafter determining its three dimensional ~~conformational~~ structure, wherein the crystallization is performed [[as]]by liquid-liquid diffusion in a capillary using equal volumes of a buffer: enzyme solution consisting of:

i) a buffer solution consisting of 28% PEG8000, 0.1 M Na-acetate, 0.1 M imidazole at a pH of 6.8 and with 5 mM $YbCl_3$ as an additive; and

ii) an enzyme solution consisting of 5 mg/ml LTA_4 hydrolase comprising the amino acid sequence of SEQ ID NO:1 in 10 mM Tris-HCl at a pH of 8, supplemented with 1 mM bestatin;

wherein the crystallization results in a LTA_4 hydrolase crystal having the space group $P2_12_12$ and the unit cell dimensions a=67.59 Å, b=133.51 Å, and c=83.40 Å and $\alpha=\beta=\gamma=90°$; and

iii) determining the atomic coordinates of said LTA_4 hydrolase crystal;

(b) identifying at least one potential inhibitor or agonist ~~compound~~ that is at least in part complementary to the LTA_4 hydrolase by the use of the atomic coordinates of the LTA_4 hydrolase crystal~~conformational structure of the crystal complex obtained in step a)~~;

(c) soaking the co-crystallized LTA_4 hydrolase obtained in step a) with a solution of ~~a compound~~the potential inhibitor or agonist identified in step b) to obtain a complex of the crystal of said LTA_4 hydrolase and said potential inhibitor or agonist ~~compound~~; and

(d) determining the atomic coordinates ~~performing X-ray crystallography~~ of the crystal complex of said LTA_4 hydrolase and said inhibitor or agonist in step (c)~~compound~~ to determine the structure thereof, thereby identifying the potential inhibitor or agonist~~compound~~ as an inhibitor or agonist of LTA_4 hydrolase~~;~~

~~wherein the crystallization results in a LTA_4 hydrolase crystal having the space group P21212 and the unit cell dimensions a=67.59 Å, b=133.51 Å, and c=83.40 Å and wherein $\alpha=\beta=\gamma=90^{o}$.~~

71. (**Previously Presented**) The method of claim 70, wherein the LTA_4 hydrolase is purified by adsorption chromatography on hydroxyapatite and anion-exchange chromatography.

72-75. (**Cancelled**)

76. (**Currently Amended**) The method of claim 70, wherein the atomic coordinates of said LTA_4 hydrolase crystal in step (a) correspond to the atomic coordinates defining atom 1 to atom 4876 as set forth in Table 9.

77. (**Cancelled**)

78. (**Currently Amended**) The method of claim 70, further comprising the step of refining the structure of the inhibitor or agonist~~said compound obtained in step d) via computer modeling using data~~ obtained in step d) via computer modeling and using this refined data~~from the X-ray crystallography in step d)~~ and repeating steps b)-d).

79. (**Previously Presented**) The method of claim 70, wherein the complex obtained in step c) comprises bestatin.

80-86. (**Cancelled**)